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Effect of the Number and Range
of GMAVs on FAV

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APPENDIX C

EFFECT OF THE NUMBER AND RANGE OF GMAVS ON FAV

The FAV is the estimate of the GMAV of a theoretical 5th percentile most-sensitive genus from the known distribution of GMAVs. In general, the FAV estimate is more certain when the range (variance) among the four lowest GMAVs is low. Similarly, the FAV estimate is more certain when the range (variance) among the P values for the four lowest GMAVs is low (this range decreases as the number of GMAVs increase). The CMC, or the acute SSO, is calculated as the FAV divided by 2. An understanding of GMAVs and FAVs can be gained from numeric examples and graphs in the following section.

TABLE C-1. FAV CALCULATION PROCEDURE {Calculations for select chemicals can be done at USEPA Region 7 Website: http://www.epa.gov/region7/water/equ.htm}

- For each genus for which one or more SMAVs are available, the GMAV should be calculated as the geometric mean of the SMAVs available for the genus.

- Order the GMAVs from high to low.

- Assign ranks, R, to the GMAVs from "1" for the lowest to "N" for the highest. If two or more GMAVs are identical, arbitrarily assign them successive ranks.

- Calculate the cumulative probability, P, for each GMAV as $R/(N+1)$.

- Select the four GMAVs which have cumulative probabilities closest to 0.05 (if there are fewer than 59 GMAVs, these will always be the four lowest GMAVs).

- Using the selected GMAVs and Ps, calculate:

$$S^2 = \frac{\Sigma((\ln GMAV)^2) - ((\Sigma(\ln GMAV))^2 / 4)}{\Sigma (P) - ((\Sigma(\sqrt{P}))^2 / 4)}$$

$$L = (\Sigma(\ln GMAV) - S(\Sigma(\sqrt{P}))) / 4$$

$$A = S(\sqrt{0.05}) + L$$

$$FAV = e^A$$

FAV Calculation Examples

The examples provided in this section are based upon an entirely hypothetical set of GMAVs. The types of outcomes illustrated are general and should apply to any dataset, but the magnitude of the changes will differ as a function of the actual number and the exact values of GMAVs. The examples illustrated in Figures C-1 and C-2 were developed from the following hypothetical

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baseline situations:

- the four lowest GMAVs are 2.5, 4.1, 9.6 and 20.3 μg/L, and

- the total number of GMAVs are either low (N = 10), intermediate (N = 20), or high (N = 40).

Baseline Results

The hypothetical baseline data will yield FAVs of 1.209, 2.223, and 5.336 μg/L for Ns of 10, 20, and 40, respectively. Clearly, the FAV is lower as the number of GMAVs decreases, even with the identical four lowest GMAVs. This is because of the increased variability (range) of the P values (a function of N) used in the calculation of the FAV (Figure C-1). Adding GMAVs to the dataset without introducing a new value into the four lowest GMAVs will always increase the FAV.

The actual FAVs calculated by the USEPA method are included in the legend and are not derived using the apparent regressions that are included simply for the sake of illustration.
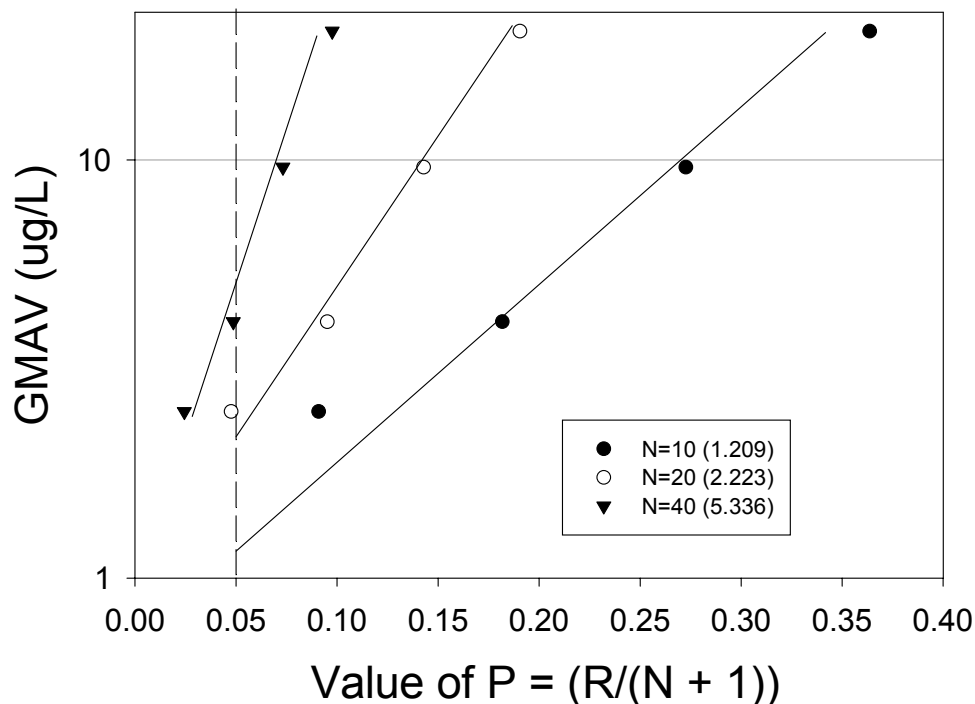
FIGURE C-1.   AN ILLUSTRATION OF THE EFFECT OF NUMBER OF GMAVS (N = 10, 20, OR 40) ON THE VALUES OF P FOR THE FOUR LOWEST GMAVS.

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Effect of GMAV Range

The hypothetical baseline data included GMAVs that ranged from 2.5 to 20.3 μg/L. The FAV calculation was shown to be influenced by the number of GMAVs through the effect of N on the range of P values (Figure C-1). The FAV is also sensitive to the range among the four lowest GMAVs. If the four lowest GMAVs were 2.5, 2.8, 3.1, and 3.9 μg/L the resultant FAVs would be 2.139, 2.422, and 2.897 μg/L for N of 10, 20, and 40, respectively (Figure C-2). Minimizing the range among the four lowest GMAVs decreases the uncertainty of the 5th percentile GMAV estimate.
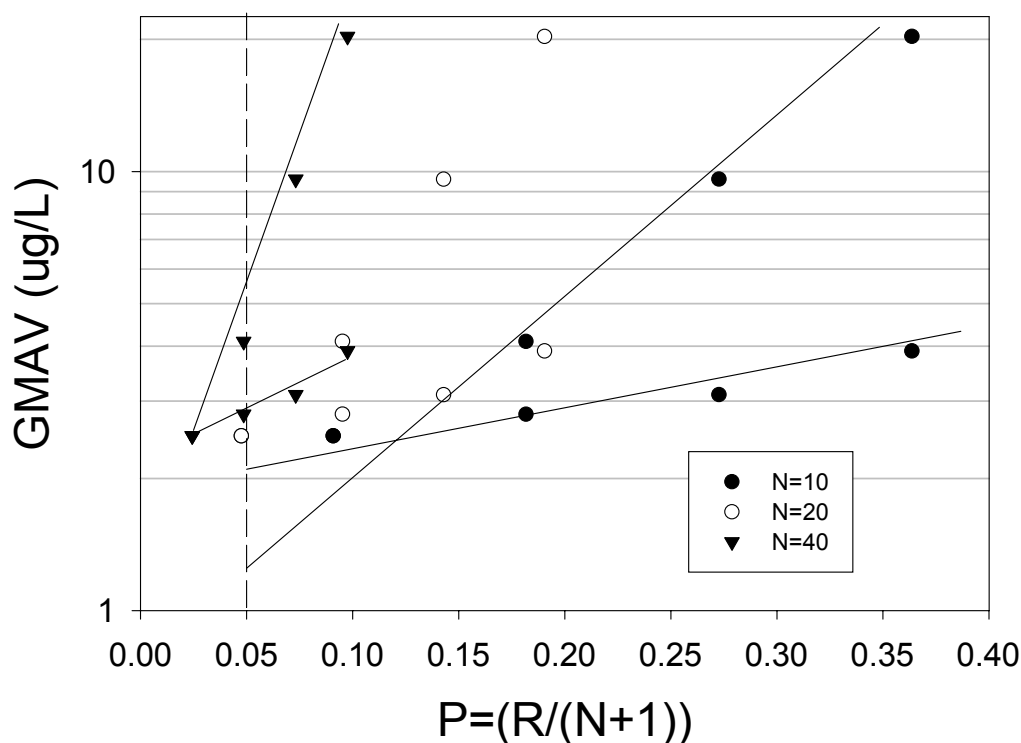

FIGURE C-2.   AN ILLUSTRATION OF THE EFFECT OF RANGE, OR VARIATION, AMONG THE FOUR LOWEST GMAVS ON THE FAV ESTIMATE.

Lines have been excluded for the case of N=20 in order to simplify the graph. Note that each dataset has a common lowest GMAV of 2.5 μg/L. The actual FAVs as computed by the USEPA procedure were 1.209, 2.223, and 5.336 for the baseline data and N of 10, 20, and 40, respectively. The actual FAVs for the narrower range of GMAVs were 2.139, 2.422, and 2.897 for N of 10, 20, and 40, respectively.

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Recalculation Procedure for FAVs

The recalculation procedure involves the addition of new data and the deletion of unsatisfactory
data (both with USEPA approval), and, if desired, the deletion from the national dataset of
nonresident and nonsurrogate species according to USEPA guidelines. Any net increase or
decrease in the number of GMAVs as a result of the addition or deletion of data from the criteria
dataset, without changing the four lowest GMAVs, will alter the FAV in a predictable direction
(Figure C-3). The influence of changing N is greater when there is a large range represented by
the four lowest GMAVs as compared to when there is a small range (Figure C-2).
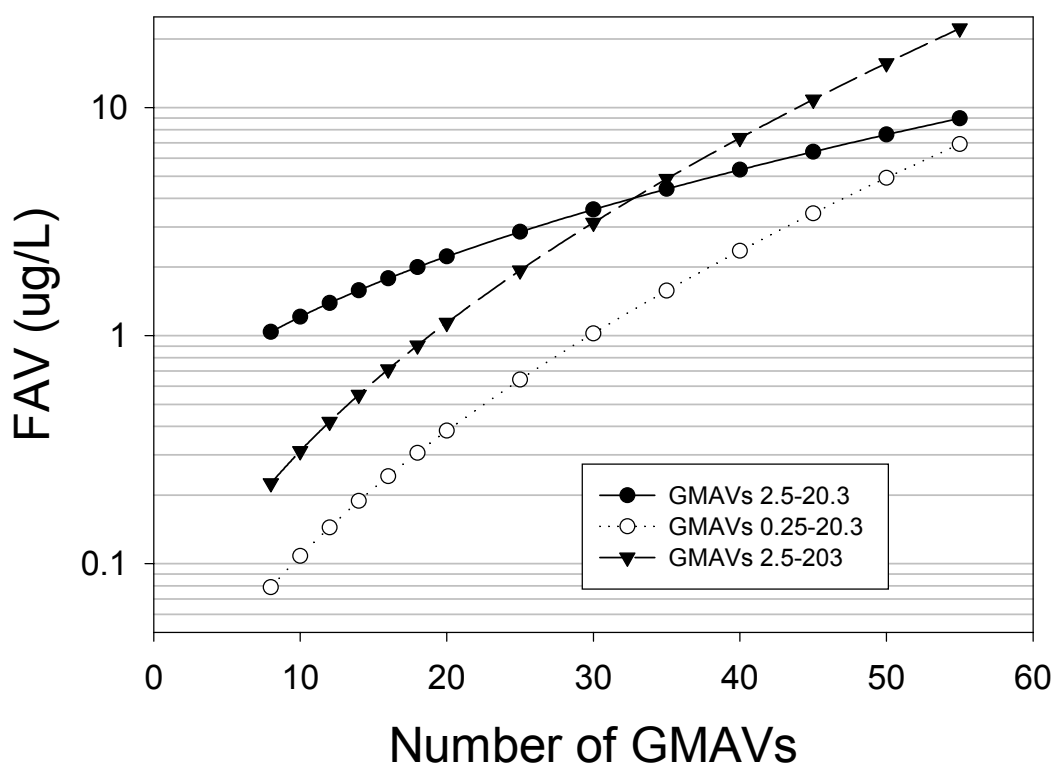
**FIGURE C-3.   ILLUSTRATION OF THE TREND IN FAV AS THE NUMBER
OF GMAVS INCREASES FROM 8 TO 55.**

The magnitude of the trend is dependent upon the range or variability among the four
lowest GMAVs (e.g., 2.5-20.3; 0.25-20.3; 2.5-203).

Recalculation with only resident species and surrogate species can provide a taxonomically more
appropriate SSO, but the procedure can have a multitude of outcomes with respect to the resultant
FAV. In addition to changes in the number of GMAVs (usually resulting in a decrease due to
deletion of nonresident and nonsurrogate species) there is also the likelihood of changes in the
four lowest GMAVs. The following three examples indicate the complexity of these changes.

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Case 1. Starting with the hypothetical baseline data (see the first paragraph in FAV Calculation Examples), reduce the total GMAVs by 20 percent and add a resident species that is more sensitive than any in the national dataset. The four lowest GMAVs are now 1.0, 2.5, 4.1, and 9.6.

Case 2. Starting with the hypothetical baseline data (see the first paragraph in FAV Calculation Examples), reduce the total GMAVs by 20 percent and delete the most sensitive species as a nonresident, nonsurrogate species. The four lowest GMAVs are now 4.1, 9.6, 20.3, and 25.0.

Case 3. Starting with the hypothetical baseline data (see the first paragraph in FAV Calculation Examples), reduce the total GMAVs by 20 percent, add a resident species that is more sensitive than any in the national dataset, and delete the two most sensitive species as nonresident, nonsurrogate species. The four lowest GMAVs are now 1.0, 9.6, 20.3, and 25.0.

TABLE C-2.   COMPARISON OF THE FAV VALUES THAT RESULT FROM THE BASELINE DATASET AND THE THREE CASES ILLUSTRATING POTENTIAL OUTCOMES OF THE RECALCULATION PROCEDURE.

	FAV Values		
	Number of GMAVs in Baseline Dataset		
	N = 10	**N = 20**	**N = 40**
Baseline	1.209	2.223	5.336
Case 1	0.4704	0.8166	1.8107
Case 2	2.2843	3.6860	7.3548
Case 3	0.4312	1.0188	3.5252

In Case 1, the FAVs are lower than the baseline for two reasons: the 20 percent lower Ns, and the addition of the new most sensitive species. Note that for the cases where the initial Ns were 20 and 40, the FAV would have to be lowered to 0.5 if the newly added most-sensitive species was recreationally, commercially, or ecological important, i.e., the FAV = $1.0 \div 2$. The same outcome would have resulted from simply adding the new "important" species data to the national dataset.

In Case 2, the FAVs are higher than the baseline, despite the 20 percent lower Ns, due to the deletion of the one most-sensitive species from the national dataset.

In Case 3, the FAVs are lower than the baseline because of the 20 percent lower Ns and the addition of the new most-sensitive species. Note that with a low initial N of 10, the FAV is lower in case 3 than in case 1, despite the loss of two of the most-sensitive species from the database in case 3; this is a result of the greater range of the GMAVs for the remaining four most-sensitive species.

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In conclusion, it is important to understand that there are several factors that can influence the FAV resulting from the recalculation procedure.

- The number of GMAVs in the initial and final datasets;

- The range or variation among the four most sensitive GMAVs in the initial and final datasets;

- Changes in the absolute values of the GMAVs for the four most sensitive species in the initial and final datasets.